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MAR 05 2002

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1. (Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe, said method comprising:

introducing a mismatch with an intended target sequence in said non-linear probe; and

conducting a hybridization reaction using said at least two homologous probes, thereby reducing the background signals of the hybridization reaction.

2. (Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous target sequences, said method comprising:

providing for an intended mismatch between at least one of the two homologous target sequences and at least one non-linear probe; and

conducting a hybridization reaction using said at least two homologous target sequences, thereby reducing the background signals of the hybridization reaction.

16. (Amended) A method of conducting a hybridization reaction comprising:

mixing a set of homologous probes for detecting at least one allelic variant of a nucleic acid, wherein at least one of said set of homologous probes is non-linear, said set of homologous probes [comprise]comprising at least one sequence completely complementary to and specific for one of the allelic variants of said nucleic acid, except for a specific mismatch located upstream, downstream or both upstream and downstream from the site of variation;

detecting variants of the nucleic acids; and

using the set of homologous probes to conduct the hybridization reaction.